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SEQUENCE LISTING TECH CENTER 1600/2900 MAR 21 2002

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<110> Lechler, Robert I.
Dorling, Anthony

<120> IMMUNOSUPPRESSION BY BLOCKING T CELL CO-STIMULATION SIGNAL 2 (B7/CD28 INTERACTION)

<130> 2292/0H795

<140> US 09/674,462

<141> 2001-05-08

<150> PCT/ GB99/01350

<151> 1999-04-30

<160> 27

<170> PatentIn Ver. 2.1

<210> 1

<211> 223

<212> PRT

<213> Sus scrofa

<400> 1

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Ser Arg Thr Trp Pro Cys Thr Ala Leu Phe Ser Leu Leu Phe Ile Pro
20 25 30

Val Phe Ser Lys Gly Met His Val Ala Gln Pro Ala Val Val Leu Ala
35 40 45

Asn Ser Arg Gly Val Ala Ser Phe Val Cys Glu Tyr Gly Ser Ala Gly
50 55 60

Lys Ala Ala Glu Val Arg Val Thr Val Leu Arg Arg Ala Gly Ser Gln
65 70 75 80

Met Thr Glu Val Cys Ala Ala Thr Tyr Thr Val Glu Asp Glu Leu Thr
85 90 95

Phe Leu Asp Asp Ser Thr Cys Thr Gly Thr Ser Thr Glu Asn Lys Val
100 105 110

Asn Leu Thr Ile Gln Gly Leu Arg Ala Val Asp Thr Gly Leu Tyr Ile
115 120 125

Cys Lys Val Glu Leu Leu Tyr Pro Pro Pro Tyr Tyr Val Gly Met Gly
 130 135 140

Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser
 145 150 155 160

Asp Phe Leu Leu Trp Ile Leu Ala Ala Val Ser Ser Gly Leu Phe Phe
 165 170 175

Tyr Ser Phe Leu Ile Thr Ala Val Ser Leu Ser Lys Met Leu Lys Lys
 180 185 190

Arg Ser Pro Leu Thr Thr Gly Val Tyr Val Lys Met Pro Pro Thr Glu
 195 200 205

Pro Glu Cys Glu Lys Gln Phe Gln Pro Tyr Phe Ile Pro Ile Asn
 210 215 220

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 <212> DNA
 <213> Sus scrofa

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 gccaacacgt cagtagtgct ggccaacacg cggggtggtg ccagctttgt gtgtgagtat 180
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 gatttcctgc tctggatcct ggcagcagtt agttcagggt tgttttttta cagcttcctc 540
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<210> 3
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 <213> Artificial Sequence

<220>
 <223> pCTLA4-Ig construct (Figure 4)

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 305 310 315 320
 Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
 325 330 335
 Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
 340 345 350
 Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
 355 360 365
 Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
 370 375 380
 Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 385 390 395 400

<210> 4
 <211> 722
 <212> DNA
 <213> Phage library

<400> 4
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 ctccagggaa ggggctggag tgggtctcag ctattcgtgg tagtggtggg agcacatact 180
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<210> 5
 <211> 240
 <212> PRT
 <213> Phage library

<210> 6
 <211> 729
 <212> DNA
 <213> Phage library

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 gctgtatctg caaatgaaca gcctgagagc cgaggacacg gccgtgtatt actgtgcaag 300
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 gccaccctca gcgtctggga cccccgggca gaggggtcacc atctcttggt ctggaagcag 480
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 caagtctggc acctcagcct ccctggccat cagtgggctc cggtcaggag atgaggctga 660
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 cctaggtgc 729

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 <211> 738
 <212> DNA
 <213> Phage library

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 ccggcagccc ccagggaagg gactggagtg gattgggtat atctattaca gtgggagcac 180
 caactacaac ccctccctca agagtcgagt caccatatca gtagacacgt ccaagaacca 240
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 caagtctggc acctcagcct ccctggccat cagtgggctc cggtcaggag atgaggctga 660
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<210> 8
 <211> 739
 <212> DNA
 <213> Phage library

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 caggcccctg gacaagggct tgagtggatg ggaataatca accctagtgg tggtagcaca 180

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caagctacgc acagaagttc cagggcagag tcaccatgac cagggacacg tccacgagca 240
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gaatggctcc ctatgtgaat acgcttgttt tttggggcca aggtaccctg gtcaccgtct 360
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tgactcagga cctgctgtg tctgtggcct tgggacagac agtcaggatc acatgccaaag 480
taggagacag cctcagaagc tattatgcaa gctggtacca gcagaagcca ggacaggccc 540
ctgtacttgt catctatggt aaaaacaacc ggccctcagg gatcccagac cgattctctg 600
gctccagctc aggaaacaca gcttccttga ccatcactgg ggctcaggcg gaagatgagg 660
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<210> 9
 <211> 729
 <212> DNA
 <213> Phage library

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tgaagatctc ctgtaagggt tctggataca gctttaccag ctactggatc ggctgggtgc 120
gccagatgcc cgggaaaggc ctggagtgga tggggatcat ctatcctggg gactctgata 180
ccagatacag cccgtccttc caaggccagg tcaccatctc agccgacaag tccatcagca 240
ccgcctacct gcagtggagc agcctgaagg cctcggacac ggccgtgtat tactgtgcaa 300
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agtctccatg ttctgtctctg catctgtagg agacagagtc accatcactt gccgggcccag 480
tcagggcatt agcagttatt tagcctggtg tcagcaaaaa ccagggaaag cccctaagct 540
cctggtctat gctgcatcca ctttgcaaag tgggggtccc tcaagggttc gcggcagtg 600
atctgggaca gaattcactc tcacaatcag cagcctgcag cctgaagatt ttgcaactta 660
ttactgtcaa cagcttaata gttaccgctt gacgttcggc caagggacca agctggaaat 720
caaacgtgc 729

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<210> 10
 <211> 240
 <212> PRT
 <213> Phage library

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
  20               25               30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
  35               40               45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
  50               55               60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

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<400> 13

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| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Ser | Leu | Lys | Ile | Ser | Cys | Lys | Gly | Ser | Gly | Tyr | Ser | Phe | Thr | Ser | Tyr |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Trp | Ile | Gly | Trp | Val | Arg | Gln | Met | Pro | Gly | Lys | Gly | Leu | Glu | Trp | Met |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Gly | Ile | Ile | Tyr | Pro | Gly | Asp | Ser | Asp | Thr | Arg | Tyr | Ser | Pro | Ser | Phe |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Gln | Gly | Gln | Val | Thr | Ile | Ser | Ala | Asp | Lys | Ser | Ile | Ser | Thr | Ala | Tyr |
| | 65 | | | | 70 | | | | | 75 | | | | | 80 |
| Leu | Gln | Trp | Ser | Ser | Leu | Lys | Ala | Ser | Asp | Thr | Ala | Val | Tyr | Tyr | Cys |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Ala | Arg | Phe | Ser | Leu | Gly | Gly | Phe | Asp | Tyr | Trp | Gly | Gln | Gly | Thr | Leu |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Val | Thr | Val | Ser | Ser | Gly | Gly | Gly | Gly | Ser | Gly | Gly | Gly | Gly | Ser | Gly |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Gly | Ser | Ala | Leu | Asp | Ile | Gln | Leu | Thr | Gln | Ser | Pro | Ser | Phe | Leu | Ser |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Ala | Ser | Val | Gly | Asp | Arg | Val | Thr | Ile | Thr | Cys | Arg | Ala | Ser | Gln | Gly |
| | 145 | | | | 150 | | | | | 155 | | | | | 160 |
| Ile | Ser | Ser | Tyr | Leu | Ala | Trp | Tyr | Gln | Gln | Lys | Pro | Gly | Lys | Ala | Pro |
| | | | | 165 | | | | | 170 | | | | | 175 | |
| Lys | Leu | Leu | Val | Tyr | Ala | Ala | Ser | Thr | Leu | Gln | Ser | Gly | Val | Pro | Ser |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Arg | Phe | Ser | Gly | Ser | Gly | Ser | Gly | Thr | Glu | Phe | Thr | Leu | Thr | Ile | Ser |
| | | 195 | | | | | 200 | | | | | 205 | | | |
| Ser | Leu | Gln | Pro | Glu | Asp | Phe | Ala | Thr | Tyr | Tyr | Cys | Gln | Gln | Leu | Asn |
| | 210 | | | | | 215 | | | | | 220 | | | | |
| Ser | Tyr | Arg | Leu | Thr | Phe | Gly | Gln | Gly | Thr | Lys | Leu | Glu | Ile | Lys | Arg |
| | 225 | | | | 230 | | | | | 235 | | | | | 240 |

<210> 14
 <211> 742
 <212> DNA
 <213> Homo sapiens

<400> 14
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 cctggccctg cactctcctg ttttttcttc tcttcacccc tgtcttctgc aaagcaatgc 180
 acgtggccca gcctgctgtg gtactggcca gcagccgagg catcgccagc tttgtgtgtg 240
 agtatgcac tccaggcaaa gccactgagg tccgggtgac agtgcttcgg caggctgaca 300
 gccagggtgac tgaagtctgt gcggcaacct acatgatggg gaatgagttg accttcctag 360
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 attctgactt cctcctctgg atccttgcag cagttagttc ggggttggtt ttttatagct 600
 ttctcctcac agctgtttct ttgagcaaaa tgctaaagaa aagaagccct cttacaacag 660
 gggcttatgt gaaaatgccc ccaacagagc cagaatgtga aaagcaattt cagccttatt 720
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<210> 15
 <211> 223
 <212> PRT
 <213> Homo sapiens

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 20 25 30
 Val Phe Cys Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala
 35 40 45
 Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly
 50 55 60
 Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln
 65 70 75 80
 Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr
 85 90 95
 Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val
 100 105 110
 Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile
 115 120 125

Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly
 130 135 140
 Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser
 145 150 155 160
 Asp Phe Leu Leu Trp Ile Leu Ala Ala Val Ser Ser Gly Leu Phe Phe
 165 170 175
 Tyr Ser Phe Leu Leu Thr Ala Val Ser Leu Ser Lys Met Leu Lys Lys
 180 185 190
 Arg Ser Pro Leu Thr Thr Gly Val Tyr Val Lys Met Pro Pro Thr Glu
 195 200 205
 Pro Glu Cys Glu Lys Gln Phe Gln Pro Tyr Phe Ile Pro Ile Asn
 210 215 220

<210> 16
 <211> 773
 <212> DNA
 <213> Homo sapiens

<400> 16
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 aggaaccgaa gacgtgtttg caaatgtccc cggcctgtgg tcaaatacgg agacaagccc 720
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<210> 17
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<400> 17
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<210> 18
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<400> 18
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<210> 19
 <211> 60
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<400> 19
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<210> 20
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<400> 20
 gagctgaaac gggcggccgc agaac 25

<210> 21
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 <212> DNA
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<220>
 <223> PCR primer

<400> 21
 ctggcctgca gcattcagat cc 22

<210> 22
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 <212> DNA
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<220>

<223> PCR primer

<400> 22

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30

<210> 23

<211> 33

<212> DNA

<213> Artificial Sequence

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<223> PCR primer

<400> 23

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33

<210> 24

<211> 76

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 24

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tccgttgect atgccc 76

<210> 25

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 25

tcgcgcctcaa gcttcgagcc aagcagcgt

29

<210> 26

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 26

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33

<210> 27

<211> 73

<212> DNA

<213> Artificial Sequence

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<223> PCR primer

<400> 27

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tgatatctac atc 73